GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 12, 2005, 09:32:54 ; Search time 485 Seconds
(without alignments)
7799.412 Million cell updates/sec

Title: US-09-721-183-4
Perfect score: 639
Sequence: 1 ccagaaccgagtttaggtcc.....cacgaatggacggaggggat 639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	639	100.0	639	5	AAD06846	Aad06846 Human bre
	2	637.4	99.7	1104	8	ABZ71575	Abz71575 Breast sp
	3	637.4	99.7	1104	12	ADF85817	Adf85817 Human bre
	4	501.8	78.5	1011	4	AAK89498	Aak89498 Human dig
	5	498.2	78.0	611	4	AAK87973	Aak87973 Human dig
	6	350.4	54.8	2360	6	ABZ22025	Abz22025 Human NIP
	7	306	47.9	307	8	ABZ71574	Abz71574 Breast sp
	8	306	47.9	307	12	ADF85816	Adf85816 Human bre
	9	99.8	15.6	766	10	ADC32261	Adc32261 Human nov
	10	99.8	15.6	1192	10	ADC30390	Adc30390 Human nov
	11	99.8	15.6	2112	10	ADB62991	Adb62991 Human cDN
c	12	75.8	11.9	503	11	ACN92793	Acn92793 Breast ca
	13	45.2	7.1	202251	11	ACN44504	Acn44504 Mouse gen
c	14	42	6.6	53522	6	AAD30228	Aad30228 Human PKD
c	15	42	6.6	53526	2	AAT94101	Aat94101 Human PKD
c	16	42	6.6	53577	2	AAT18551	Aat18551 Human pol
c	17	42	6.6	53577	2	AAT94108	Aat94108 Human PKD
	18	39.2	6.1	540	13	ACN47094	Acn47094 Cotton pr
c	19	38.4	6.0	2000	8	ADA71938	Ada71938 Rice gene
c	20	37.8	5.9	79640	13	ABD33007	Abd33007 Mouse can
	21	37.4	5.9	1000	3	AAA02484	Aaa02484 Human col
	22	37.4	5.9	118584	10	ADC87623	Adc87623 Human GPC
	23	37.4	5.9	349999	10	ADC87010	Adc87010 Human GPC
c	24	37.2	5.8	1038	2	AAQ51019	Aaq51019 EBV VCA-p
c	25	37.2	5.8	172281	12	ADN12161	Adn12161 Epstein-B
c	26	36.6	5.7	10732	3	AAA10594	Aaa10594 Gene enco
	27	36.2	5.7	203132	13	ABD33364	Abd33364 Murine ca
	28	35.6	5.6	2230	11	ADM02845	Adm02845 Human cDN
	29	35.6	5.6	7444	8	ABT19632	Abt19632 Aspergill
	30	35.6	5.6	7496	8	ABT17818	Abt17818 Aspergill
	31	35.6	5.6	8456	13	ADR84410	Adr84410 Aspergill
c	32	35.2	5.5	134442	13	ABD32824	Abd32824 Mouse can
	33	35	5.5	1527	5	AAS68546	Aas68546 DNA encod
c	34	35	5.5	1620	5	AAS68547	Aas68547 DNA encod
c	35	35	5.5	2178	5	AAS86106	Aas86106 DNA encod
c	36	35	5.5	26047	11	ACN44246	Acn44246 Human gen
c	37	34.8	5.4	500	6	ABN15750	Abn15750 Human gen
c	38	34.8	5.4	500	13	ACN78840	Acn78840 Human GDM
c	39	34.8	5.4	505	12	ACH73908	Ach73908 Human gen
	40	34.8	5.4	1967	4	AAI13118	Aai13118 Probe #30
	41	34.8	5.4	1967	4	ABA54817	Aba54817 Human foe
	42	34.8	5.4	1967	4	AAI34469	Aai34469 Probe #31
	43	34.8	5.4	1967	4	ABA44363	Aba44363 Human bre
	44	34.8	5.4	1967	4	ABA24581	Aba24581 Probe #30
	45	34.8	5.4	1967	4	AAK28545	Aak28545 Human bon

ALIGNMENTS

RESULT 1
AAD06846
ID AAD06846 standard; DNA; 639 BP.
XX
AC AAD06846;
XX
DT 06-AUG-2001 (first entry)
XX
DE Human breast cancer specific gene-4 (BCSG-4).
XX
KW Human; breast cancer specific gene-4; BCSG-4; cytostatic; vaccine;
KW breast cancer; therapeutic; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200137779-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US032056.
XX
PR 23-NOV-1999; 99US-0166973P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Salceda S, Cafferkey R, Recipon H, Sun Y;
XX
DR WPI; 2001-367602/38.
XX
PT Novel breast cancer specific gene for diagnosing, monitoring, staging,
PT imaging, preventing and treating cancers, particularly breast cancer.
XX
PS Claim 1; Page 51; 66pp; English.
XX
CC The invention relates human breast cancer specific genes (BCSG's) and
CC their corresponding proteins. BCSG is useful for diagnosing, staging,
CC monitoring, imaging, preventing and treating breast cancers. BCSG is also
CC useful for inducing an immune response against a target cell expressing
CC BCSG. The invention also provide methods for detecting genetic lesions or
CC mutations in BCSG, thereby determining if a human with the genetic lesion
CC is at risk for breast cancer or has breast cancer. BCSG antibodies
CC labelled with paramagnetic ions or radioisotopes is useful for imaging
CC breast cancers, while BCSG antibodies conjugated to a cytotoxic agent is

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CC   useful for treating breast cancer. BCSG is useful in the rational design
CC   of new therapeutics for imaging and treating cancers. BCSG is also used
CC   in gene therapy. The present DNA sequence is human breast cancer specific
CC   gene-4 (BCSG-4) or Gene ID 173388
XX
SQ   Sequence 639 BP; 146 A; 148 C; 168 G; 177 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 639;  DB 5;  Length 639;
  Best Local Similarity  100.0%;  Pred. No. 7.4e-188;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCAGAACCGAGTTTAGGTCCAGGTTCTCGTTCTGGCAAATCTTTCTCCTTACCTTCTTCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCAGAACCGAGTTTAGGTCCAGGTTCTCGTTCTGGCAAATCTTTCTCCTTACCTTCTTCC 60

Qy         61 TCCACCCCTCCACCTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCACCCCTCCACCTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAG 120

Qy        121 GCAGGCCTAACTAGGTACCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCAGGCCTAACTAGGTACCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGC 180

Qy        181 TGGGTTCCAGCCACTTGTAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGGAGCAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGTTCCAGCCACTTGTAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGGAGCAAC 240

Qy        241 TGCTACAGAGGTAAATATGATTAACTTTACATTCCATCTTTCGTCTGCTCCCAAACTTAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCTACAGAGGTAAATATGATTAACTTTACATTCCATCTTTCGTCTGCTCCCAAACTTAA 300

Qy        301 CAGCAGGTAATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCAGGTAATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGCA 360

Qy        361 AGAGATCTGAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGAGATCTGAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCA 420

Qy        421 TTTCAATTATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCTTGGGGGCTGTCTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTTCAATTATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCTTGGGGGCTGTCTT 480

Qy        481 AGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGAGTTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGAGTTG 540

Qy        541 GAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGGTGGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGGTGGCT 600

Qy        601 GGGAGAAGGGAGGGGTGGTCACGAATGGACGGAGGGGAT 639
              |||||||||||||||||||||||||||||||||||||||
Db        601 GGGAGAAGGGAGGGGTGGTCACGAATGGACGGAGGGGAT 639


RESULT 2
ABZ71575
ID   ABZ71575 standard; cDNA; 1104 BP.
XX
AC   ABZ71575;
XX
DT   04-APR-2003  (first entry)
XX
DE   Breast specific nucleic acid # SEQ ID 35.
XX
KW   Human; breast specific nucleic acid; breast cancer; gene therapy;
KW   cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200288375-A2.
XX
PD   07-NOV-2002.
XX
PF   29-OCT-2001; 2001WO-US051318.
XX
PR   27-OCT-2000; 2000US-0243805P.
XX
PA   (DIAD-) DIADEXUS INC.
XX
PI   Sun Y,  Recipon H,  Salceda S,  Liu C,  Turner LR;
XX
DR   WPI; 2003-156692/15.
XX
PT   New breast-specific nucleic acids and polypeptides, useful for
PT   identifying, diagnosing, monitoring, staging, imaging, and treating
PT   breast cancer and non-cancerous disease states in breast tissues.
XX
PS   1 b; Page 174-175; 269pp; English.
XX
CC   The invention relates to breast-specific nucleic acid and polypeptide
CC   sequences. The activity of sequences of the invention may be described as
CC   cytostatic. The breast-specific nucleic acids, polypeptides and
CC   compositions comprising them are useful for identifying, diagnosing,
CC   monitoring, staging, imaging, and treating breast cancer and non-
CC   cancerous disease states in breast tissue. They are also useful for
CC   identifying breast tissue, for monitoring, identifying or designing
CC   agonists and antagonists of the polypeptides, in gene therapy, in
CC   producing transgenic animals and cells, for producing engineered breast
CC   tissue for treatment and research, and as elements in an array or
CC   computer program for pattern recognition of breast disorders. The nucleic
CC   acids may be used as hybridisation probes to detect, characterise and
CC   quantify hybridising nucleic acids in, and isolate hybridising nucleic
CC   acids from, both genomic and transcript-derived nucleic acid samples. The
CC   sequences given in records ABZ71541-ABZ71693 represent breast-specific
CC   nucleic acid sequences of the invention
XX
SQ   Sequence 1104 BP; 294 A; 229 C; 293 G; 288 T; 0 U; 0 Other;

  Query Match            99.7%;  Score 637.4;  DB 8;  Length 1104;
  Best Local Similarity  99.8%;  Pred. No. 3.1e-187;
  Matches  638;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCAGAACCGAGTTTAGGTCCAGGTTCTCGTTCTGGCAAATCTTTCTCCTTACCTTCTTCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 CCAGAACCGAGTTTAGGTCCAGGTTCTCGTTCTGGCAAATCTTTCTCCTTACCTTCTTCC 525

Qy         61 TCCACCCCTCCACCTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 TCCACCCCTCCACCTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAG 585

Qy        121 GCAGGCCTAACTAGGTACCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 GCAGGCCTAACTAGGTACCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGC 645

Qy        181 TGGGTTCCAGCCACTTGTAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGGAGCAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 TGGGTTCCAGCCACTTGTAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGGAGCAAC 705

Qy        241 TGCTACAGAGGTAAATATGATTAACTTTACATTCCATCTTTCGTCTGCTCCCAAACTTAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TGCTACAGAGGTAAATATGATTAACTTTACATTCCATCTTTCGTCTGCTCCCAAACTTAA 765

Qy        301 CAGCAGGTAATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CAGCAGGTAATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGCA 825

Qy        361 AGAGATCTGAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AGAGATCTGAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCA 885

Qy        421 TTTCAATTATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCTTGGGGGCTGTCTT 480
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 TTTGAATTATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCTTGGGGGCTGTCTT 945
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Qy        481 AGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGAGTTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 AGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGAGTTG 1005

Qy        541 GAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGGTGGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 GAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGGTGGCT 1065

Qy        601 GGGAGAAGGGAGGGGTGGTCACGAATGGACGGAGGGGAT 639
              |||||||||||||||||||||||||||||||||||||||
Db       1066 GGGAGAAGGGAGGGGTGGTCACGAATGGACGGAGGGGAT 1104
```

RESULT 3
ADF85817
ID ADF85817 standard; cDNA; 1104 BP.
XX
AC ADF85817;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human breast specific nucleic acid (BSNA) cDNA, SEQ ID NO:35.
XX
KW Human; breast specific nucleic acid; BSNA; breast cancer; metastasis;
KW diagnosis; monitoring; staging; imaging; immunotherapy; vaccine;
KW cytostatic; gene therapy; transgenic animal; tissue engineering; ss.
XX
OS Homo sapiens.
XX
PN WO2003099989-A2.
XX
PD 04-DEC-2003.
XX
PF 22-MAY-2002; 2002WO-US016307.
XX
PR 22-MAY-2002; 2002WO-US016307.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Sun Y, Recipon H, Salceda S, Liu C, Turner LR;
XX
DR WPI; 2004-042804/04.
XX
PT New breast specific nucleic acid molecules and proteins, useful for
PT identifying, diagnosing, monitoring, staging, imaging and treating breast
PT cancer and non-cancerous disease states in breast tissue.
XX
PS Claim 1; SEQ ID NO 35; 269pp; English.
XX
CC The invention relates to 153 breast specific nucleic acids (BSNA;
CC ADF85783-ADF85935) and to breast specific proteins (BSP; ADF85936-
CC ADF86004). The invention also encompasses sequences at least 60%
CC identical to the BSNAs and BSPs of the invention; vectors and host cells
CC comprising a BSNA; the recombinant production of BSPs using a host cell
CC comprising a BSNA; an antibody specific for a BSP; methods of detecting
CC an BSNA or BSP; a method for diagnosing or monitoring the presence and
CC metastases of breast cancer in a patient; a kit for detecting the risk or
CC presence of cancer in a patient; a method for the treatment of breast
CC cancer via the administration of a BSNA or BSP to raise an immune
CC response against the breast cancer cell expressing the BSNA or BSP; and a
CC vaccine composition comprising a BSNA or BSP. The BSNAs, BSPs, methods
CC and compositions of the present invention are useful for diagnosing,
CC monitoring, staging, imaging, and treating breast cancer and breast
CC cancer metastases, and also non-cancerous disease states in breast
CC tissue. The BSNAs and BSPs are also useful for producing transgenic
CC animals and cells, for producing engineered breast tissue for treatment
CC and research, or for identifying breast tissue for breast cell
CC differentiation and development. The present sequence represents a
CC specifically claimed breast specific nucleic acid (BSNA). Note: 113 BSPs
CC are claimed in the invention; however, only 69 of these (ADF85936-
CC ADF86004) are given in the specification.
XX
SQ Sequence 1104 BP; 294 A; 229 C; 293 G; 288 T; 0 U; 0 Other;

Query Match 99.7%; Score 637.4; DB 12; Length 1104;
Best Local Similarity 99.8%; Pred. No. 3.1e-187;
Matches 638; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 CCAGAACCGAGTTTAGGTCCAGGTTCTCGTTCTGGCAAATCTTTCTCCTTACCTTCTTCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 CCAGAACCGAGTTTAGGTCCAGGTTCTCGTTCTGGCAAATCTTTCTCCTTACCTTCTTCC 525

Qy         61 TCCACCCCTCCACCTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 TCCACCCCTCCACCTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAG 585

Qy        121 GCAGGCCTAACTAGGTACCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 GCAGGCCTAACTAGGTACCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGC 645

Qy        181 TGGGTTCCAGCCACTTGTAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGGAGCAAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 TGGGTTCCAGCCACTTGTAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGGAGCAAC 705

Qy        241 TGCTACAGAGGTAAATATGATTAACTTTACATTCCATCTTTCGTCTGCTCCCAAACTTAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 TGCTACAGAGGTAAATATGATTAACTTTACATTCCATCTTTCGTCTGCTCCCAAACTTAA 765

Qy        301 CAGCAGGTAATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGCA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 CAGCAGGTAATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGCA 825

Qy        361 AGAGATCTGAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AGAGATCTGAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCA 885

Qy        421 TTTCAATTATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCTTGGGGGCTGTCTT 480
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        886 TTTGAATTATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCTTGGGGGCTGTCTT 945

Qy        481 AGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGAGTTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        946 AGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGAGTTG 1005

Qy        541 GAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGGTGGCT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1006 GAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGGTGGCT 1065

Qy        601 GGGAGAAGGGAGGGGTGGTCACGAATGGACGGAGGGGAT 639
              |||||||||||||||||||||||||||||||||||||||
Db       1066 GGGAGAAGGGAGGGGTGGTCACGAATGGACGGAGGGGAT 1104
```

RESULT 4
AAK89498
ID AAK89498 standard; DNA; 1011 BP.
XX
AC AAK89498;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 3074.
XX
KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ds.
XX
OS Homo sapiens.
XX
PN WO200155314-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001324.
XX
PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
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PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-502630/55.
XX
PT Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognozing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX

```
PS   Disclosure; SEQ ID NO 3074; 986pp; English.
XX
CC   The present invention provides the protein and coding sequences of a
CC   number of human digestive system antigens. These can be used in the
CC   diagnosis, treatment and prevention of digestive system disorders,
CC   including cancer, Meckel's diverticulum, bacterial or parasitic
CC   infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC   ulcerative colitis. The present sequence is a genomic DNA fragment
CC   encoding a digestive system antigen of the invention
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SQ   Sequence 1011 BP; 270 A; 220 C; 248 G; 273 T; 0 U; 0 Other;

  Query Match             78.5%;  Score 501.8;  DB 4;  Length 1011;
  Best Local Similarity   99.6%;  Pred. No. 4.4e-145;
  Matches  503;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCAGAACCGAGTTTAGGTCCAGGTTCTCGTTCTGGCAAATCTTTCTCCTTACCTTCTTCC 60
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Db        482 CCAGAACCGAGTTTAGGTCCAGGTTCTCGTTCTGGCAAATCTTTCTCCTTACCTTCTTCC 541

Qy         61 TCCACCCCTCCACCTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAG 120
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        542 TCCACCCCTCCACTTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAG 601

Qy        121 GCAGGCCTAACTAGGTACCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGC 180
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        602 GCAGGCCTAACTAGGTAGCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGC 661

Qy        181 TGGGTTCCAGCCACTTGTAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGGAGCAAC 240
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Db        662 TGGGTTCCAGCCACTTGTAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGGAGCAAC 721

Qy        241 TGCTACAGAGGTAAATATGATTAACTTTACATTCCATCTTTCGTCTGCTCCCAAACTTAA 300
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Qy        361 AGAGATCTGAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCA 420
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Qy        421 TTTCAATTATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCTTGGGGGCTGTCTT 480
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Qy        481 AGGGTCAGGGAGATTGCAGAAGCAC 505
              |||||||||||||||||||||||||
Db        962 AGGGTCAGGGAGATTGCAGAAGCAC 986


RESULT 5
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ID   AAK87973 standard; cDNA; 611 BP.
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AC   AAK87973;
XX
DT   05-NOV-2001  (first entry)
XX
DE   Human digestive system antigen coding sequence SEQ ID NO: 289.
XX
KW   Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW   ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW   digestive system disorder; Meckel's diverticulum; ss.
XX
OS   Homo sapiens.
XX
PN   WO200155314-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001324.
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XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-502630/55.
DR   P-PSDB; AAM92200.
XX
PT   Polynucleotides encoding digestive system antigens, useful for
PT   diagnosing, treating, preventing and/or prognozing disorders of the
PT   digestive system, particularly cancer and cancer metastases.
XX
PS   Claim 1; SEQ ID NO 289; 986pp; English.
XX
CC   The present invention provides the protein and coding sequences of a
CC   number of human digestive system antigens. These can be used in the
CC   diagnosis, treatment and prevention of digestive system disorders,
CC   including cancer, Meckel's diverticulum, bacterial or parasitic
CC   infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC   ulcerative colitis. The present sequence is a cDNA encoding a digestive
CC   system antigen of the invention
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SQ   Sequence 611 BP; 133 A; 144 C; 153 G; 177 T; 0 U; 4 Other;

  Query Match             78.0%;  Score 498.2;  DB 4;  Length 611;
  Best Local Similarity   98.6%;  Pred. No. 4.5e-144;
  Matches  555;  Conservative    0;  Mismatches    3;  Indels    5;  Gaps    5;

Qy          1 CCAGAACCGAGTTTAGGTCCAGGTTCTCGTTCTGGCAAATCTTTCTCCTTACCTTCTTCC 60
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Qy         61 TCCACCCCTCCACCTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TCCACCCCTCCACCTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAG 121

Qy        121 GCAGGCCTAACTAGGTACCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 GCAGGCCTAACTAGGTACCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGC 181

Qy        181 TGGGTTCCAGCCACTTGTAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGGAGCAAC 240
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Db        182 TGGGTTCCAGCCACTTGTAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGGAGCAAC 241

Qy        241 TGCTACAGAGGTAAATATGATTAACTTTACATTCCATCTTTCGTCTGCTCCCAAACTTAA 300
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Db        242 TGCTACAGAGGTAAATATGATTAACTTTACATTCCATCTTTCGTCTGCTCCCAAACTTAA 301

Qy        301 CAGCAGGTAATCTGC-TTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGC 359
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        302 CAGCAGGTAATCTGCTTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGC 361

Qy        360 AAGAGATCTGAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTC 419
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Db        362 AAGAGATCTGAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTC 421

Qy        420 ATTTCAATTATTCTTACCTACTATTCAGTTCCCTT-GATCTTTTCTTCTTGGGGGCTGTC 478
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Db        422 ATTTCAATTATTCTTACCTACTATTCAGTTCCCTTGGATCTTTTCTTCTTGGGGGCTGTC 481

Qy        479 TTAGGGTCAGGG-AGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGA-GACATGGGGA 536
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Db        482 TTAGGGTCAGGGTGGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGGACATGGGGA 541

Qy        537 G-TTGGAGCTGAAGGAGGAATGG 558
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Db        542 GTTTGGAGCTGAAGGAGGGATTG 564


RESULT 6
ABZ22025
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XX
AC   ABZ22025;
XX
DT   10-MAR-2003  (first entry)
XX
DE   Human NIP2 associated protein encoding cDNA SEQ ID NO:3.
XX
KW   Human; nuclear cap binding protein interacting protein 2; NCBP; NIP2;
KW   NCBP interacting protein; NIP2 associated protein; NIP2 AP; cancer; gene;
```

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OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  a
FT                   /product= "NIP2 AP"
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PN   CN1343688-A.
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PD   10-APR-2002.
XX
PF   19-SEP-2000; 2000CN-00125281.
XX
PR   19-SEP-2000; 2000CN-00125281.
XX
PA   (SHAN-) SHANGHAI CITY INST TUMORS.
XX
PI   Gu J,  Yang S;
XX
DR   WPI; 2002-548862/59.
DR   P-PSDB; ABP56265.
XX
PT   Novel human NIP2 associated protein.
XX
PS   Claim 5; Page 14-16 (Disclosure); 25pp; Chinese.
XX
CC   The present sequence encodes a human nuclear cap binding protein (NCBP)
CC   interacting protein 2 (NIP2) associated protein (I). NIP2 AP can be used
CC   for treating diseases such as cancer. The present sequence represents a
CC   PCR primer for NIP2 AP, which is used in an example from the present
CC   invention
XX
SQ   Sequence 2360 BP; 569 A; 562 C; 621 G; 608 T; 0 U; 0 Other;

  Query Match             54.8%;  Score 350.4;  DB 6;  Length 2360;
  Best Local Similarity   97.0%;  Pred. No. 8.2e-98;
  Matches  357;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy        228 TAGGTGGAGCAACTGCTACAGAGGTAAATATGATTAACTTTACATTCCATCTTTCGTCTG 287
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Qy        288 CTCCCAAACTTAACAGCAGGTAATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATC 347
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        348 TGTATAGGAGGCAAGAGATCTGAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAA 407
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Qy        408 TTACTGTTCTTCATTTCAATTATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCT 467
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Qy        468 TGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAG 527
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Qy        528 ACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACG 587
              |||||||||||||||||||||||||||||||||||||||||||||||| |     |
Db        458 ACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGATTGCTTCC 517

Qy        588 TGTGAGGG 595
              || |  ||
Db        518 TGAGGAGG 525


RESULT 7
ABZ71574
ID   ABZ71574 standard; cDNA; 307 BP.
XX
AC   ABZ71574;
XX
DT   04-APR-2003  (first entry)
XX
DE   Breast specific nucleic acid # SEQ ID 34.
XX
KW   Human; breast specific nucleic acid; breast cancer; gene therapy;
KW   cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200288375-A2.
XX
PD   07-NOV-2002.
XX
PF   29-OCT-2001; 2001WO-US051318.
XX
PR   27-OCT-2000; 2000US-0243805P.
XX
PA   (DIAD-) DIADEXUS INC.
XX
PI   Sun Y,  Recipon H,  Salceda S,  Liu C,  Turner LR;
XX
DR   WPI; 2003-156692/15.
XX
PT   New breast-specific nucleic acids and polypeptides, useful for
PT   identifying, diagnosing, monitoring, staging, imaging, and treating
PT   breast cancer and non-cancerous disease states in breast tissues.
XX
PS   1 b; Page 174; 269pp; English.
XX
CC   The invention relates to breast-specific nucleic acid and polypeptide
CC   sequences. The activity of sequences of the invention may be described as
CC   cytostatic. The breast-specific nucleic acids, polypeptides and
CC   compositions comprising them are useful for identifying, diagnosing,
CC   monitoring, staging, imaging, and treating breast cancer and non-
CC   cancerous disease states in breast tissue. They are also useful for
CC   identifying breast tissue, for monitoring, identifying or designing
CC   agonists and antagonists of the polypeptides, in gene therapy, in
CC   producing transgenic animals and cells, for producing engineered breast
CC   tissue for treatment and research, and as elements in an array or
CC   computer program for pattern recognition of breast disorders. The nucleic
CC   acids may be used as hybridisation probes to detect, characterise and
CC   quantify hybridising nucleic acids in, and isolate hybridising nucleic
CC   acids from, both genomic and transcript-derived nucleic acid samples. The
CC   sequences given in records ABZ71541-ABZ71693 represent breast-specific
CC   nucleic acid sequences of the invention
XX
SQ   Sequence 307 BP; 73 A; 53 C; 99 G; 81 T; 0 U; 1 Other;

  Query Match             47.9%;  Score 306;  DB 8;  Length 307;
  Best Local Similarity   99.7%;  Pred. No. 1.9e-84;
  Matches  306;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        333 GGTAAGAGAAGCATCTGTATAGGAGGCAAGAGATCTGAGTCCTTTTGAAGGCCTATCCTC 392
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 GGTAAGAGAAGCATCTGTATAGGAGGCNAGAGATCTGAGTCCTTTTGAAGGCCTATCCTC 60

Qy        393 TGCTCTGTATCTCAATTACTGTTCTTCATTTCAATTATTCTTACCTACTATTCAGTTCCC 452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCTCTGTATCTCAATTACTGTTCTTCATTTCAATTATTCTTACCTACTATTCAGTTCCC 120

Qy        453 TTGATCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACT 512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTGATCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACT 180

Qy        513 AGGAGCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATT 572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGAGCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATT 240

Qy        573 CCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACGG 632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACGG 300
```

```
Qy        633 AGGGGAT 639
              |||||||
Db        301 AGGGGAT 307


RESULT 8
ADF85816
ID   ADF85816 standard; cDNA; 307 BP.
XX
AC   ADF85816;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human breast specific nucleic acid (BSNA) cDNA, SEQ ID NO:34.
XX
KW   Human; breast specific nucleic acid; BSNA; breast cancer; metastasis;
KW   diagnosis; monitoring; staging; imaging; immunotherapy; vaccine;
KW   cytostatic; gene therapy; transgenic animal; tissue engineering; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003099989-A2.
XX
PD   04-DEC-2003.
XX
PF   22-MAY-2002; 2002WO-US016307.
XX
PR   22-MAY-2002; 2002WO-US016307.
XX
PA   (DIAD-) DIADEXUS INC.
XX
PI   Sun Y,  Recipon H,  Salceda S,  Liu C,  Turner LR;
XX
DR   WPI; 2004-042804/04.
XX
PT   New breast specific nucleic acid molecules and proteins, useful for
PT   identifying, diagnosing, monitoring, staging, imaging and treating breast
PT   cancer and non-cancerous disease states in breast tissue.
XX
PS   Claim 1; SEQ ID NO 34; 269pp; English.
XX
CC   The invention relates to 153 breast specific nucleic acids (BSNA;
CC   ADF85783-ADF85935) and to breast specific proteins (BSP; ADF85936-
CC   ADF86004). The invention also encompasses sequences at least 60%
CC   identical to the BSNAs and BSPs of the invention; vectors and host cells
CC   comprising a BSNA; the recombinant production of BSPs using a host cell
CC   comprising a BSNA; an antibody specific for a BSP; methods of detecting
CC   an BSNA or BSP; a method for diagnosing or monitoring the presence and
CC   metastases of breast cancer in a patient; a kit for detecting the risk or
CC   presence of cancer in a patient; a method for the treatment of breast
CC   cancer via the administration of a BSNA or BSP to raise an immune
CC   response against the breast cancer cell expressing the BSNA or BSP; and a
CC   vaccine composition comprising a BSNA or BSP. The BSNAs, BSPs, methods
CC   and compositions of the present invention are useful for diagnosing,
CC   monitoring, staging, imaging, and treating breast cancer and breast
CC   cancer metastases, and also non-cancerous disease states in breast
CC   tissue. The BSNAs and BSPs are also useful for producing transgenic
CC   animals and cells, for producing engineered breast tissue for treatment
CC   and research, or for identifying breast tissue for breast cell
CC   differentiation and development. The present sequence represents a
CC   specifically claimed breast specific nucleic acid (BSNA). Note: 113 BSPs
CC   are claimed in the invention; however, only 69 of these (ADF85936-
CC   ADF86004) are given in the specification.
XX
SQ   Sequence 307 BP; 73 A; 53 C; 99 G; 81 T; 0 U; 1 Other;

  Query Match             47.9%;  Score 306;  DB 12;  Length 307;
  Best Local Similarity   99.7%;  Pred. No. 1.9e-84;
  Matches  306;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        333 GGTAAGAGAAGCATCTGTATAGGAGGCAAGAGATCTGAGTCCTTTTGAAGGCCTATCCTC 392
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||

Db          1 GGTAAGAGAAGCATCTGTATAGGAGGCNAGAGATCTGAGTCCTTTTGAAGGCCTATCCTC 60

Qy        393 TGCTCTGTATCTCAATTACTGTTCTTCATTTCAATTATTCTTACCTACTATTCAGTTCCC 452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCTCTGTATCTCAATTACTGTTCTTCATTTCAATTATTCTTACCTACTATTCAGTTCCC 120

Qy        453 TTGATCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACT 512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTGATCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACT 180

Qy        513 AGGAGCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATT 572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGAGCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATT 240

Qy        573 CCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACGG 632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACGG 300

Qy        633 AGGGGAT 639
              |||||||
Db        301 AGGGGAT 307


RESULT 9
ADC32261
ID   ADC32261 standard; cDNA; 766 BP.
XX
AC   ADC32261;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human novel cDNA contig sequence, SEQ ID NO:2343.
XX
KW   Human; diagnostic; drug screening; forensics; gene mapping;
KW   biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW   neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW   ulcers; osteoporosis; autoimmune disease; cancer;
KW   molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW   neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW   antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003029271-A2.
XX
PD   10-APR-2003.
XX
PF   24-SEP-2002; 2002WO-US030474.
XX
PR   24-SEP-2001; 2001US-0324631P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang TY,  Zhang J,  Ren F,  Xue AJ,  Zhao QA,  Wang J,  Wehrman T;
PI   Zhou P,  Ghosh M,  Wang D,  Ma Y,  Asundi V,  Wang Z,  Weng G;
PI   Haley-Vicente D,  Drmanac RT;
XX
DR   WPI; 2003-371981/35.
DR   P-PSDB; ADC33028.
XX
PT   New polynucleotide and polypeptide useful for diagnosing, preventing or
PT   treating conditions such as neurodegenerative diseases, anemias, platelet
PT   disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT   cancer.
XX
PS   Example 2; SEQ ID NO 2343; 1185pp; English.
XX
CC   The invention relates to 971 novel human cDNA sequences (ADC29919-
CC   ADC30889)and the polypeptides they encode (ADC30890-ADC31860). The
CC   invention also relates to nucleic acid sequences over 99% identical with
CC   the novel human cDNAs. The invention additionally encompasses expression
CC   vectors and host cells comprising a nucleic acid of the invention; the
```

CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of peventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a human contig
CC sequence used in an example of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 766 BP; 200 A; 169 C; 239 G; 158 T; 0 U; 0 Other;

Query Match 15.6%; Score 99.8; DB 10; Length 766;
Best Local Similarity 89.9%; Pred. No. 4e-20;
Matches 107; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 477 TCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGA 536
Db 135 TGTTGGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGA 194

Qy 537 GTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGG 595
Db 195 GTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGATTGCTTCCTGAGGAGG 253

RESULT 10
ADC30390
ID ADC30390 standard; cDNA; 1192 BP.
XX
AC ADC30390;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human novel cDNA sequence, SEQ ID NO:472.
XX
KW Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003029271-A2.
XX
PD 10-APR-2003.
XX
PF 24-SEP-2002; 2002WO-US030474.
XX
PR 24-SEP-2001; 2001US-0324631P.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI Haley-Vicente D, Drmanac RT;
XX
DR WPI; 2003-371981/35.
DR P-PSDB; ADC31361.
XX
PT New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.
XX
PS Claim 1; SEQ ID NO 472; 1185pp; English.
XX
CC The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30889)and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of peventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1192 BP; 318 A; 274 C; 342 G; 258 T; 0 U; 0 Other;

Query Match 15.6%; Score 99.8; DB 10; Length 1192;
Best Local Similarity 89.9%; Pred. No. 5e-20;
Matches 107; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 477 TCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGA 536
Db 129 TGTTGGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGA 188

Qy 537 GTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGG 595
Db 189 GTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGATTGCTTCCTGAGGAGG 247

RESULT 11
ADB62991
ID ADB62991 standard; cDNA; 2112 BP.
XX
AC ADB62991;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human cDNA encoding clone PROST20063430.
XX

```
KW   Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
KW   tissue regeneration; cell regeneration; membrane protein;
KW   signal transduction-related protein; transcription-related protein;
KW   osteoporosis; neurological disease; cancer; tumour.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             126. .1199
FT                   /*tag= a
FT                   /product= "Clone PROST20063430 protein"
XX
PN   EP1308459-A2.
XX
PD   07-MAY-2003.
XX
PF   28-MAR-2002; 2002EP-00007401.
XX
PR   05-NOV-2001; 2001JP-00379298.
PR   25-JAN-2002; 2002US-00350978.
XX
PA   (HELI-) HELIX RES INST.
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Sugiyama T,  Otsuki T,  Wakamatsu A,  Sato H,  Ishii S;
PI   Yamamoto J,  Isono Y,  Hio Y,  Otsuka K,  Nagai K,  Irie R,  Tamechika I;
PI   Seki N,  Yoshikawa T,  Otsuka M,  Nagahari K,  Masuho Y;
XX
DR   WPI; 2003-450961/43.
DR   P-PSDB; ADB64961.
XX
PT   New polynucleotides and polypeptides, useful for developing a diagnostic
PT   marker or medicines for regulation of their expression and activity, or
PT   as targets of gene therapy.
XX
PS   Claim 1; Page; 222pp; English.
XX
CC   The invention discloses a polynucleotide comprising a sequence selected
CC   from 1970 fully defined nucleotide sequences which encode novel
CC   polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC   or its partial peptide, an antibody binding to the polypeptide or peptide
CC   of the polynucleotide, immunologically assaying the polypeptide or
CC   peptide of the polynucleotide by contacting the polypeptide or peptide
CC   with the antibody of the encoded protein, and observing the binding
CC   between the two, a transformant carrying the polynucleotide in an
CC   expressible manner and an antisense polynucleotide. The oligonucleotide
CC   is useful as a primer for synthesising the polynucleotide, or as a probe
CC   for detecting the polynucleotide. The polynucleotides and encoded
CC   proteins are useful as pharmaceutical agents and many disease-related
CC   genes may be included in them, for developing a diagnostic marker or
CC   medicines for regulation of their expression and activity, or as targets
CC   of gene therapy. The genes are involved in tissue and/or cell
CC   regeneration. Membrane proteins, signal transduction-related proteins,
CC   transcription-related proteins, disease-related proteins and genes
CC   encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC   neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC   the activity or expression of the encoded protein to treat diseases. The
CC   sequence presented is a cDNA of the invention. Note: Some of the sequence
CC   data for this patent is not represented in the printed specification, but
CC   is based on sequence information supplied by the European Patent Office.
XX
SQ   Sequence 2112 BP; 497 A; 515 C; 573 G; 527 T; 0 U; 0 Other;

  Query Match            15.6%;  Score 99.8;  DB 10;  Length 2112;
  Best Local Similarity   89.9%;  Pred. No. 6.7e-20;
  Matches  107;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy        477 TCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGA 536
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TGTTGGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGA 220

Qy        537 GTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGG 595
              |||||||||||||||||||||||||||||||||||||||| |     | || |  ||

Db        221 GTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGATTGCTTCCTGAGGAGG 279


RESULT 12
ACN92793/c
ID   ACN92793 standard; DNA; 503 BP.
XX
AC   ACN92793;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Breast cancer related marker, seq id 13943.
XX
KW   Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
XX
OS   Homo sapiens.
XX
PN   US2003099974-A1.
XX
PD   29-MAY-2003.
XX
PF   18-JUL-2002; 2002US-00198846.
XX
PR   18-JUL-2001; 2001US-0306220P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lillie J,  Xu Y,  Wang Y,  Steinmann K;
XX
DR   WPI; 2003-787014/74.
XX
PT   Novel isolated polypeptide associated with breast cancer, useful for
PT   detecting presence of polypeptide in sample, as a marker for breast
PT   cancer.
XX
PS   Disclosure; SEQ ID NO 13943; 36pp; English.
XX
CC   The invention relates to an isolated polypeptide (I) associated with
CC   breast cancer which is encoded by a nucleic acid molecule comprising a
CC   nucleotide sequence (S1). Further disclosed is an antibody that binds to
CC   the polypeptide of the invention. The activity of the polypeptide of the
CC   invention may be described as cytostatic. The antibody is useful for
CC   detecting the presence of (I) in a sample. Nucleic acid molecules of the
CC   invention are useful in the detection of breast tumours. (I) is useful as
CC   a marker for breast cancer and in breast cancer therapy. Sequences given
CC   in records ACN78851-ACN92934 represent nucleic acid markers associated
CC   with breast cancer. Note: The sequence listing does not form part of the
CC   specification but may be obtained in electronic format from the USPTO web
CC   site at seqdata.uspto.gov/sequence.html?DocID=20030099974
XX
SQ   Sequence 503 BP; 126 A; 134 C; 104 G; 134 T; 0 U; 5 Other;

  Query Match            11.9%;  Score 75.8;  DB 11;  Length 503;
  Best Local Similarity   97.5%;  Pred. No. 9.5e-13;
  Matches   77;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        561 GGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTC 620
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||| ||||||||||
Db        499 GGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGGTGGCTGGAAGAAGGTAGGGGTGGTC 440

Qy        621 ACGAATGGACGGAGGGGAT 639
              ||||||||||||||||||||
Db        439 ACGAATGGACGGAGGGGAT 421


RESULT 13
ACN44504
ID   ACN44504 standard; DNA; 202251 BP.
XX
AC   ACN44504;
XX
DT   18-NOV-2004  (first entry)
XX
```

```
DE   Mouse genomic sequence mCG20408.
XX
KW   Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
XX
OS   Mus musculus.
XX
PN   WO2003073826-A2.
XX
PD   12-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-US006235.
XX
PR   01-MAR-2002; 2002US-00087192.
XX
PA   (SAGR-) SAGRES DISCOVERY.
XX
PI   Morris DW;
XX
DR   WPI; 2003-328604/31.
XX
PT   Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT   comprises a nucleotide sequence.
XX
PS   Claim 1; SEQ ID NO 985; 0pp; English.
XX
CC   The present invention relates to novel DNA and protein sequences which
CC   are associated with carcinomas. The sequences are useful for: (i) for
CC   screening drug candidates; (ii) for screening of bioactive agent capable
CC   of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC   a bioactive agent capable of modulating the activity of CAP; (iv) for
CC   evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC   carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC   carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC   (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC   determining Carcinoma Associated (CA) gene copy number. In addition, the
CC   CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC   carcinoma including lymphoma. The present sequence is one such CA coding
CC   sequence. Note: This patent is an equivalent to basic patent
CC   US2002182586A1, for which no sequence data was published
XX
SQ   Sequence 202251 BP; 51742 A; 46659 C; 46432 G; 53759 T; 0 U; 3659 Other;

  Query Match             7.1%;  Score 45.2;  DB 11;  Length 202251;
  Best Local Similarity   52.7%;  Pred. No. 0.064;
  Matches   98;  Conservative    0;  Mismatches   88;  Indels    0;  Gaps    0;

Qy        452 CTTGATCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAAC 511
              | |||  || |   | | |||          | |||  |     |||| |||| ||| |
Db     140383 CCTGACATTGTGGACCTTGGGAGAAGACAGAGATCACAGTAGCAGCAGCAGCAGCAGCAG 140442

Qy        512 TAGGAGCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAAT 571
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Db     140443 CAGCAGGAGAAAGAGGAGGAGGGGGGAAGGAGAAGGAGGAAGAGGAGGAGGGGGAAGGAG 140502

Qy        572 TCCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACG 631
                |  ||||| | |  || | ||   |||| | |  | || ||    |||||| |
Db     140503 AAGGAGGAAGAGGAGGAGGAAGAGGGGGAAGGAGGAAGAGGAGGAGGAAGAGAATGGAGG 140562

Qy        632 GAGGGG 637
                || ||
Db     140563 AAGAGG 140568


RESULT 14
AAD30228/c
ID   AAD30228 standard; DNA; 53522 BP.
XX
AC   AAD30228;
XX
DT   17-MAY-2002  (first entry)
XX
DE   Human PKD1 gene.
XX
KW   Human; PKD1 gene; autosomal dominant polycystic kidney disease; ADPKD;
KW   acquired cystic disease; transgenic animal; chromosome 16; ds.
XX
OS   Homo sapiens.
XX
PN   WO200206529-A2.
XX
PD   24-JAN-2002.
XX
PF   13-JUL-2001; 2001WO-US022035.
XX
PR   13-JUL-2000; 2000US-0218261P.
PR   13-APR-2001; 2001US-0283691P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Germino GG,  Watnick TJ,  Phakdeekitcharoen B;
XX
DR   WPI; 2002-179805/23.
XX
PT   Novel primer for diagnosing polycystic kidney disease-associated
PT   disorder, comprises regions having sequence that selectively hybridizes
PT   to polycystic kidney disease gene sequence.
XX
PS   Claim 20; Page 127-156; 192pp; English.
XX
CC   The present invention relates to compositions and methods useful for the
CC   identification and detection of polycystic kidney disease (PKD1) gene
CC   mutations. The invention also relates to primers comprising a 5' region
CC   having a sequence that selectively hybridises to a PKD1 gene sequence and
CC   optionally, to a PKD1 homologue sequence and an adjacent 3' region having
CC   a sequence that selectively hybridises to a PKD1 gene sequence and not to
CC   a PKD1 homologue sequence. Primer pairs of the invention are useful for
CC   detecting the presence or absence of a mutation in a PKD1 polynucleotide
CC   in a sample, for identifying a subject at risk for a PKD1-associated
CC   disorder such as autosomal dominant polycystic kidney disease (ADPKD) or
CC   acquired cystic disease and for diagnosing a PKD1- associated disorder in
CC   a subject. They are useful for selectively amplifying a region of a PKD1
CC   gene. PKD1 DNA fragments are useful detecting the presence of a mutant
CC   PKD1 polynucleotide in a sample, as a probe for an amplification
CC   reaction, in hybridisation or amplification assays of biological samples
CC   to detect abnormalities of PKD1 expression and for engineering transgenic
CC   animals. The present sequence is human PKD1 gene located on chromosome 16
XX
SQ   Sequence 53522 BP; 8486 A; 17664 C; 15766 G; 11606 T; 0 U; 0 Other;

  Query Match             6.6%;  Score 42;  DB 6;  Length 53522;
  Best Local Similarity   52.9%;  Pred. No. 0.32;
  Matches   90;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy        469 GGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGA 528
              ||||   |    ||||   | | ||      | || |  || |   |||| ||    |||
Db      34691 GGGGAGGGGAGGAGGGGAGGAGGGAGGAGGGGAGGAGGAGGAGGGGAGGAGGGAGGAGG 34632

Qy        529 CATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGT 588
              | | || |  ||||  |  ||  | | || |||| | || |         | | ||||
Db      34631 GAGGAGGGGGAGGAGGAGGGGGGAGGAGGGGAGGAGGGAGGAGGGGAGGAGGGGGACAG 34572

Qy        589 GTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACGGAGGGGA 638
              | | ||  ||   ||||| ||||||   ||  | ||  ||| || | |||
Db      34571 GAGGGGAGGGGGAGGAGAGGGGAGGAAGGGGGAGGAGGGGAGGGGGAGGA 34522


RESULT 15
AAT94101/c
ID   AAT94101 standard; DNA; 53526 BP.
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AC   AAT94101;
XX
DT   25-MAR-2003  (revised)
DT   01-JUN-1998  (first entry)
XX
DE   Human PKD1 gene.
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XX
KW Human; polycystic kidney disease 1; PKD1; treatment;
KW autosomal dominant polycystic kidney disease; APKD; ss.
XX
OS Homo sapiens.
XX
PN WO9744457-A1.
XX
PD 27-NOV-1997.
XX
PF 22-MAY-1997; 97WO-US008799.
XX
PR 24-MAY-1996; 96US-00655360.
PR 04-JUN-1996; 96US-00658136.
XX
PA (GENZ) GENZYME CORP.
XX
PI Klinger K, Burn T, Connors T, Dackowski W, Germino G, Qian F;
XX
DR WPI; 1998-018511/02.
XX
PT Human polycystic kidney disease gene, PKD1 - useful to treat and diagnose
PT human autosomal or adult onset polycystic kidney disease.
XX
PS Claim 2; Page 90-118; 257pp; English.
XX
CC The present sequence is the human polycystic kidney disease 1 (PKD1)
CC gene. The PKD1 gene or polypeptide may be used to treat autosomal
CC dominant polycystic kidney disease (APKD), and identify carriers of
CC mutant PKD1 genes, i.e. subjects susceptible to APKD. Antibodies (Ab)
CC that distinguish between normal and mutant PKD1 sequences can also be
CC used in diagnostic tests. Anti-PKD1 Ab may also be used to perform
CC subcellular and histochemical localisation studies, and to block the
CC function of PKD1. Ab are also useful in rational drug design studies to
CC identify and test inhibitors of PKD1. Sense and antisense sequences
CC derived from the PKD1 gene may used for detection and therapy. (Updated
CC on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 53526 BP; 8486 A; 17665 C; 15768 G; 11607 T; 0 U; 0 Other;

Query Match 6.6%; Score 42; DB 2; Length 53526;
Best Local Similarity 52.9%; Pred. No. 0.32;
Matches 90; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

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Qy        469 GGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGA 528
              ||||   |    ||||   | | ||     | || |  || |   |||| ||    |||
Db      34695 GGGGAGGGGAGGAGGGGAGGAGGGAGGAGGGGAGGAGGAGGAGGGGGAGGAGGGAGGAGG 34636

Qy        529 CATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGT 588
              | | || |  ||||  |  ||  | | || |||| | || |         | | ||||
Db      34635 GAGGAGGGGGAGGAGGAGGGGGGAGGAGGGGAGGAGGGAGGAGGGGAGGAGGGGGGACAG 34576

Qy        589 GTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACGGAGGGGA 638
              | | ||  ||   ||||| ||||||   ||  | ||  ||| || | |||
Db      34575 GAGGGGAGGGGGAGGAGAGGGGAGGAAGGGGGAGGAGGGGAGGGGGAGGA 34526
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Search completed: October 12, 2005, 09:44:04
Job time : 492 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 12, 2005, 09:32:49 ; Search time 168 Seconds
(without alignments)
6223.695 Million cell updates/sec

Title: US-09-721-183-4
Perfect score: 639
Sequence: 1 ccagaaccgagtttaggtcc.....cacgaatggacggaggggat 639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	45.2	7.1	7218	1	US-08-232-463-14	Sequence 14, Appl
c	2	42	6.6	53526	3	US-08-658-136-2	Sequence 2, Appli
c	3	42	6.6	53577	3	US-08-658-136-1	Sequence 1, Appli
	4	39.8	6.2	7218	1	US-08-232-463-14	Sequence 14, Appl
	5	38.2	6.0	8279	4	US-09-949-016-13478	Sequence 13478, A
c	6	37.2	5.8	1038	1	US-08-031-148-3	Sequence 3, Appli
c	7	37.2	5.8	1038	3	US-08-415-838-3	Sequence 3, Appli
c	8	37.2	5.8	1038	3	US-09-205-169-3	Sequence 3, Appli
c	9	36.4	5.7	79350	4	US-09-949-016-12467	Sequence 12467, A
c	10	36.4	5.7	79351	4	US-09-949-016-16275	Sequence 16275, A
c	11	36.4	5.7	247781	4	US-09-949-016-14193	Sequence 14193, A
	12	36.2	5.7	149971	4	US-09-949-016-13590	Sequence 13590, A
	13	36	5.6	462	4	US-09-621-976-15621	Sequence 15621, A
	14	35.4	5.5	120727	4	US-09-949-016-15787	Sequence 15787, A
	15	35.4	5.5	120727	4	US-09-949-016-15788	Sequence 15788, A
	16	35.2	5.5	18955	4	US-09-949-016-13343	Sequence 13343, A
	17	35.2	5.5	30678	4	US-09-949-016-12818	Sequence 12818, A
c	18	34.8	5.4	500	4	US-09-866-108A-15742	Sequence 15742, A
c	19	34.8	5.4	1141	4	US-09-806-708B-22	Sequence 22, Appl
c	20	34.8	5.4	231129	4	US-09-949-016-16110	Sequence 16110, A
c	21	34.8	5.4	266293	4	US-09-949-016-11934	Sequence 11934, A
	22	34.6	5.4	9052	4	US-09-949-016-13662	Sequence 13662, A
c	23	34.6	5.4	23802	4	US-09-949-016-12107	Sequence 12107, A
c	24	34.6	5.4	23803	4	US-09-949-016-15878	Sequence 15878, A
	25	34.6	5.4	174029	4	US-09-949-016-12610	Sequence 12610, A
	26	34.6	5.4	174030	4	US-09-949-016-13880	Sequence 13880, A
	27	34.4	5.4	289	3	US-09-007-005-17	Sequence 17, Appl
	28	34.4	5.4	289	3	US-09-244-796-17	Sequence 17, Appl
	29	34.4	5.4	3614	4	US-09-221-013A-9	Sequence 9, Appli
	30	34.2	5.4	601	4	US-09-949-016-103065	Sequence 103065,
	31	34.2	5.4	601	4	US-09-949-016-103140	Sequence 103140,
	32	34.2	5.4	601	4	US-09-949-016-187952	Sequence 187952,
	33	34.2	5.4	15907	4	US-09-949-016-16818	Sequence 16818, A
	34	34.2	5.4	300598	4	US-09-949-016-11868	Sequence 11868, A
	35	34.2	5.4	302604	4	US-09-949-016-14588	Sequence 14588, A
	36	34.2	5.4	302604	4	US-09-949-016-14589	Sequence 14589, A
	37	34.2	5.4	308362	4	US-09-949-016-17119	Sequence 17119, A
	38	34	5.3	6585	4	US-09-949-016-14470	Sequence 14470, A
c	39	33.8	5.3	3293	4	US-09-949-016-4658	Sequence 4658, Ap
c	40	33.8	5.3	3314	4	US-09-949-016-836	Sequence 836, App
c	41	33.8	5.3	4544	4	US-08-956-171E-517	Sequence 517, App
c	42	33.8	5.3	4544	4	US-08-781-986A-517	Sequence 517, App
c	43	33.8	5.3	31440	4	US-09-949-016-12578	Sequence 12578, A
c	44	33.8	5.3	31444	4	US-09-949-016-16400	Sequence 16400, A
	45	33.8	5.3	78649	4	US-09-949-016-14619	Sequence 14619, A

ALIGNMENTS

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RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             7.1%;  Score 45.2;  DB 1;  Length 7218;
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  Best Local Similarity   3.1%;  Pred. No. 0.0023;
  Matches    5;  Conservative  111;  Mismatches   44;  Indels    0;  Gaps    0;

Qy        479 TTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGAGT 538
              || ||  |:::::::  : ::::: :  ::::  ::::: ::    :::: : ::::::
Db       1442 TTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1383

Qy        539 TGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGGTGG 598
               ::::  :::::::::: :: :::: ::::::      ::: ::::: : : ::::: ::
Db       1382 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1323

Qy        599 CTGGGAGAAGGGAGGGGTGGTCACGAATGGACGGAGGGGA 638
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Db       1322 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1283


RESULT 2
US-08-658-136-2/c
; Sequence 2, Application US/08658136
; Patent No. 6071717
;  GENERAL INFORMATION:
;    APPLICANT:  KLINGER, KATHERINE W
;    APPLICANT:  LANDES, GREGORY M
;    APPLICANT:  BURN, TIMOTHY C
;    APPLICANT:  CONNORS, TIMOTHY D
;    APPLICANT:  DACKOWSKI, WILLIAM
;    APPLICANT:  GERMINO, GREGORY
;    APPLICANT:  QIAN, FENG
;    TITLE OF INVENTION:  POLYCYSTIC KIDNEY DISEASE GENE
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GENZYME CORPORATION
;      STREET:  ONE MOUNTAIN ROAD
;      CITY:  FRAMINGHAM
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  01701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/658,136
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LASSEN, ELIZABETH
;      REGISTRATION NUMBER:  31,845
;      REFERENCE/DOCKET NUMBER:  GEN4-17.8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  508-872-8400
;      TELEFAX:  508-872-5415
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  53526 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-658-136-2

  Query Match             6.6%;  Score 42;  DB 3;  Length 53526;
  Best Local Similarity   52.9%;  Pred. No. 0.075;
  Matches   90;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy        469 GGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGA 528
              ||||   |   ||||   | | ||      | || |  || |   |||| ||    |||
Db      34695 GGGGAGGGGAGGAGGGGAGGAGGGAGGAGGGGAGGAGGAGGGGAGGAGGGAGGAGG 34636

Qy        529 CATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGT 588
              | | || |  ||||  |  ||  | | || |||| | || |        | | ||||
Db      34635 GAGGAGGGGGAGGAGGAGGGGGGAGGAGGGGAGGAGGGAGGAGGGGAGGAGGGGGACAG 34576

Qy        589 GTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACGGAGGGGA 638
              | | ||  ||   ||||| ||||||   ||  | ||  ||| || | |||
Db      34575 GAGGGGAGGGGGAGGAGAGGGGAGGAAGGGGGAGGAGGGGAGGGGGAGGA 34526


RESULT 3
US-08-658-136-1/c
; Sequence 1, Application US/08658136
; Patent No. 6071717
;  GENERAL INFORMATION:
;    APPLICANT:  KLINGER, KATHERINE W
;    APPLICANT:  LANDES, GREGORY M
;    APPLICANT:  BURN, TIMOTHY C
;    APPLICANT:  CONNORS, TIMOTHY D
;    APPLICANT:  DACKOWSKI, WILLIAM
;    APPLICANT:  GERMINO, GREGORY
;    APPLICANT:  QIAN, FENG
;    TITLE OF INVENTION:  POLYCYSTIC KIDNEY DISEASE GENE
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  GENZYME CORPORATION
;      STREET:  ONE MOUNTAIN ROAD
;      CITY:  FRAMINGHAM
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  01701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/658,136
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LASSEN, ELIZABETH
;      REGISTRATION NUMBER:  31,845
;      REFERENCE/DOCKET NUMBER:  GEN4-17.8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  508-872-8400
;      TELEFAX:  508-872-5415
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  53577 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-658-136-1

  Query Match             6.6%;  Score 42;  DB 3;  Length 53577;
  Best Local Similarity   52.9%;  Pred. No. 0.075;
  Matches   90;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy        469 GGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGA 528
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Db      34690 GGGGAGGGAGGAGGGGAGGAGGGAGGAGGGGAGGAGGAGGAGGGGGAGGAGGGAGGAGG 34631

Qy        529 CATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGT 588
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Db      34630 GAGGAGGGGGAGGAGGAGGGGGGAGGAGGGGAGGAGGGAGGAGGGGAGGAGGGGGACAG 34571

Qy        589 GTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACGGAGGGGA 638
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Db      34570 GAGGGGAGGGGGAGGAGAGGGGAGGAAGGGGGAGGAGGGGAGGGGGAGGA 34521


RESULT 4
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
```

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;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             6.2%;  Score 39.8;  DB 1;  Length 7218;
  Best Local Similarity   5.4%;  Pred. No. 0.12;
  Matches   17;  Conservative  167;  Mismatches  129;  Indels    0;  Gaps    0;

Qy          7 CCGAGTTTAGGTCCAGGTTCTCGTTCTGGCAAATCTTTCTCCTTACCTTCTTCCTCCACC 66
              ||||| || | | |||||    |         ||:::::::::: :::::::::::: ::
Db       1033 CCGAGCTTGGCTGCAGGTCGAGGGAGCTTGCGATYYYYYYYYYYYYYYYYYYYYYYYYYY 1092

Qy         67 CCTCCACCTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAGGCAGGC 126
              ::::: ::: : :: : ::::::::::  :: ::::::  :::  :         :   :
Db       1093 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1152

Qy        127 CTAACTAGGTACCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGCTGGGTT 186
              ::  ::   : :: :::::::  :::: ::: :  :  ::  :   ::: ::   ::
Db       1153 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1212

Qy        187 CCAGCCACTTGTAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGGAGCAACTGCTAC 246
              ::  :: ::: :  : :    : ::::::: :::  :::: :   :    :  :: :: :
Db       1213 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1272

Qy        247 AGAGGTAAATATGATTAACTTTACATTCCATCTTTCGTCTGCTCCCAAACTTAACAGCAG 306
                  :  : :  ::  :::: : :::: :::::: ::: :::::   :::  :  :
Db       1273 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1332

Qy        307 GTAATCTGCTTCT 319
              :  ::: :::::
Db       1333 YYYYYYYYYYYYY 1345
```

```
RESULT 5
US-09-949-016-13478
; Sequence 13478, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13478
;   LENGTH: 8279
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-13478

  Query Match             6.0%;  Score 38.2;  DB 4;  Length 8279;
  Best Local Similarity   52.1%;  Pred. No. 0.42;
  Matches   85;  Conservative    0;  Mismatches   78;  Indels    0;  Gaps    0;

Qy        469 GGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGA 528
              ||||||     |  ||   ||| |   | ||| |  |||| | | ||   ||    | |
Db       1215 GGGGGCATAGGTGTGGAAGGGGTGGGGGAAGAGGGGCCAGGAGTGGGGTGAGAAGAGGGG 1274

Qy        529 CATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGT 588
                | |  |||      |  | |   |||  || ||      || | |   ||||   ||| |
Db       1275 AAAGAAGAGGATAGGAGGGACAGGGACAGGGAGAGGCCAGGAATGGGTAGGAAGGGAAGA 1334

Qy        589 GTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACG 631
                ||||  ||  ||||  ||||||||| | | | ||  || ||
Db       1335 CAGAGGAGGGGCGGGACGAGGGAGGGGCGATGAAGAGGGGCCG 1377


RESULT 6
US-08-031-148-3/c
; Sequence 3, Application US/08031148
; Patent No. 5424398
;  GENERAL INFORMATION:
;    APPLICANT:  Middeldorp, Jaap Michiel.
;    TITLE OF INVENTION:  Peptides and nucleic acid sequences
;    TITLE OF INVENTION:  related to the Epstein-Barr virus.
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Akzo Pharma
;      STREET:  1330-A Piccard Drive
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850-4377
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patentin Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/031,148
;      FILING DATE:  19930312
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 92200721.6
;      FILING DATE:  13-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bobrowicz, Donna
```

```
;       REGISTRATION NUMBER:  32,196
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  1038 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  double
;       TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;       ORGANISM:  Epstein-Barr virus
US-08-031-148-3

  Query Match             5.8%;  Score 37.2;  DB 1;  Length 1038;
  Best Local Similarity   52.6%;  Pred. No. 0.27;
  Matches   81;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy        457 TCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGA 516
              |||||||  ||||  || |  |   ||  | ||||  | |       | | ||    |
Db        468 TCTTTTCCGCTTGTTGGATCGCGAGGGAGCGGGGACGTAGTCTGCCCGCAAGTGGGATCC 409

Qy        517 GCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCT 576
              | ||    ||| || |||  |  || |   || ||||   |||| |   ||| |  ||
Db        408 GTAGTAAGGAGGCACGGGTGGAGGGGGGCCAAAGAGGCCCGGCAAGCCAAAGTAGGCCGG 349

Qy        577 AGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGG 610
              ||| | |   | ||| ||||||  ||    || |
Db        348 AGGGGGGTGTGGGTGGGGGTGGTAGGTGTGAGCG 315


RESULT 7
US-08-415-838-3/c
; Sequence 3, Application US/08415838
; Patent No. 6008327
;  GENERAL INFORMATION:
;    APPLICANT:  Middeldorp, Jaap Michiel.
;    TITLE OF INVENTION:  Peptides and nucleic acid sequences
;    TITLE OF INVENTION:  related to the Epstein-Barr virus.
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Akzo-No. 6008327el Patent Department
;      STREET:  1300 Piccard Drive, Suite 206
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patentin Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/415,838
;      FILING DATE:  03-APR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 92200721.6
;      FILING DATE:  13-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gormley, Mary E.
;      REGISTRATION NUMBER:  34,409
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1038 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Epstein-Barr virus
US-08-415-838-3

  Query Match             5.8%;  Score 37.2;  DB 3;  Length 1038;
  Best Local Similarity   52.6%;  Pred. No. 0.27;
  Matches   81;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy        457 TCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGA 516
              |||||||  ||||  || |  |   ||  | ||||  | |       | | ||    |
Db        468 TCTTTTCCGCTTGTTGGATCGCGAGGGAGCGGGGACGTAGTCTGCCCGCAAGTGGGATCC 409

Qy        517 GCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCT 576
              | ||    ||| || |||  |  || |   || ||||   |||| |   ||| |  ||
Db        408 GTAGTAAGGAGGCACGGGTGGAGGGGGGCCAAAGAGGCCCGGCAAGCCAAAGTAGGCCGG 349

Qy        577 AGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGG 610
              ||| | |   | ||| ||||||  ||    || |
Db        348 AGGGGGGTGTGGGTGGGGGTGGTAGGTGTGAGCG 315


RESULT 8
US-09-205-169-3/c
; Sequence 3, Application US/09205169
; Patent No. 6365717
;  GENERAL INFORMATION:
;       APPLICANT: Middeldorp, Jaap Michiel.
;       TITLE OF INVENTION: Peptides and nucleic acid sequences
;                           related to the Epstein-Barr virus.
;       NUMBER OF SEQUENCES: 22
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Akzo-No. 6365717el Patent Department
;            STREET: 1300 Piccard Drive, Suite 206
;            CITY: Rockville
;            STATE: Maryland
;            COUNTRY: USA
;            ZIP: 20850
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: Patentin Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/205,169
;            FILING DATE: 04-Dec-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/415,838
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Gormley, Mary E.
;            REGISTRATION NUMBER: 34,409
;  INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1038 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: unknown
;       MOLECULE TYPE: DNA (genomic)
;       ORIGINAL SOURCE:
;            ORGANISM: Epstein-Barr virus
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-205-169-3

  Query Match             5.8%;  Score 37.2;  DB 3;  Length 1038;
  Best Local Similarity   52.6%;  Pred. No. 0.27;
  Matches   81;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy        457 TCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGA 516
              |||||||  ||||  || |  |   ||  | ||||  | |       | | ||    |
Db        468 TCTTTTCCGCTTGTTGGATCGCGAGGGAGCGGGGACGTAGTCTGCCCGCAAGTGGGATCC 409

Qy        517 GCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCT 576
              | ||    ||| || |||  |  || |   || ||||   |||| |   ||| |  ||
Db        408 GTAGTAAGGAGGCACGGGTGGAGGGGGGCCAAAGAGGCCCGGCAAGCCAAAGTAGGCCGG 349

Qy        577 AGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGG 610
              ||| | |   | ||| ||||||  ||    || |
Db        348 AGGGGGGTGTGGGTGGGGGTGGTAGGTGTGAGCG 315
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RESULT 9
US-09-949-016-12467/c
; Sequence 12467, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12467
;   LENGTH: 79350
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(79350)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12467

  Query Match             5.7%;  Score 36.4;  DB 4;  Length 79350;
  Best Local Similarity   55.6%;  Pred. No. 5.6;
  Matches   70;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy        351 ATAGGAGGCAAGAGATCTGAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTA 410
              | ||||    |  ||| | ||       ||||||  | |        ||| | ||||  |
Db      65064 AAAGGAACAGAAGGATGTCAGAAGAAGAGAAGGCATGTGTGTGTGTCTCTCTCTCTCTCT 65005

Qy        411 CTGTTCTTCATTTCAATTATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCTTGG 470
              || |  |   ||||  ||||| ||| ||  | ||||| ||| |||   ||  ||| | |
Db      65004 CTCTCTTCATTTTCTCTTATTGTTAACTCATTTTCAGCTCCTTTGGGTTTCACTTTTGGA 64945

Qy        471 GGGCTG 476
              |  |||
Db      64944 GCACTG 64939


RESULT 10
US-09-949-016-16275/c
; Sequence 16275, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16275
;   LENGTH: 79351
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(79351)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16275

  Query Match             5.7%;  Score 36.4;  DB 4;  Length 79351;
  Best Local Similarity   55.6%;  Pred. No. 5.6;
  Matches   70;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy        351 ATAGGAGGCAAGAGATCTGAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTA 410
              | ||||    |  ||| | ||       ||||||  | |        ||| | ||||  |
Db      65064 AAAGGAACAGAAGGATGTCAGAAGAAGAGAAGGCATGTGTGTGTGTCTCTCTCTCTCTCT 65005

Qy        411 CTGTTCTTCATTTCAATTATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCTTGG 470
              || |  |   ||||  ||||| ||| ||  | ||||| ||| |||   ||  ||| | |
Db      65004 CTCTCTTCATTTTCTCTTATTGTTAACTCATTTTCAGCTCCTTTGGGTTTCACTTTTGGA 64945

Qy        471 GGGCTG 476
              |  |||
Db      64944 GCACTG 64939


RESULT 11
US-09-949-016-14193/c
; Sequence 14193, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14193
;   LENGTH: 247781
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(247781)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14193

  Query Match             5.7%;  Score 36.4;  DB 4;  Length 247781;
  Best Local Similarity   51.9%;  Pred. No. 11;
  Matches   82;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy        481 AGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGAGTTG 540
              |||   |||  ||    || || |  || |  ||||| ||       || | | ||||  |
Db     126708 AGGAGGAGGAGGAGGAGGAGGAAGAGGAAGAGGAGAAGGAGGAGGAGAGGAGGAGGAG 126649

Qy        541 GAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGGTGGCT 600
              ||   | |||||||   | |||| ||||       ||| || || |       | |
Db     126648 GAAGAGGAGGAGGAGAAGGAGGAAGAAGAGGAGGAGAGGAGAAGAAGAAGAGAAGGAGGA 126589

Qy        601 GGGAGAAGGGAGGGGTGGTCACGAATGGACGGAGGGGA 638
              ||  || |    ||  |   | ||   |  ||||||||
Db     126588 GGAGGAGGAAGAGGAGGAGGAAGAGAAGGAGGAGGGGA 126551


RESULT 12
US-09-949-016-13590
; Sequence 13590, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13590
;   LENGTH: 149971
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(149971)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13590

  Query Match             5.7%;  Score 36.2;  DB 4;  Length 149971;
  Best Local Similarity   54.0%;  Pred. No. 9.4;
  Matches   74;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy        376 TTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCATTTCAATTATTCTTA 435
              | || |  |||    ||   | | |  ||   | | | |  |||||  || ||||| |||
Db     134382 TCTGGACTCCTTATATCCTTTTTTTTCCTGTTTAATTTTCATTCATAGCACTTATTATTA 134441

Qy        436 CCTACTATTCAGTTCCCTTGATCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATT 495
              ||| ||| | ||    |||  |||||     |   | ||  ||   |   || |||| |
Db     134442 TCTAATATGCTGTATATTTGTACTTTTTAAAATTTTGTCTTCCTACTGCAAAGTGAGAAT 134501

Qy        496 GCAGAAGCACCAGAACT 512
              ||  || ||  ||| |
Db     134502 CCATGAGGACAGGAATT 134518


RESULT 13
US-09-621-976-15621
; Sequence 15621, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 15621
;   LENGTH: 462
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-15621

  Query Match             5.6%;  Score 36;  DB 4;  Length 462;
  Best Local Similarity   53.6%;  Pred. No. 0.41;
  Matches   75;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy        498 AGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATG 557
              || |||    ||   |||| | ||  |  || ||| | | || ||||   ||||||| |
Db         32 AGGAGCCAGTGAGACAGGAAAAACCTAGTAACGTGGTGTGATGAAGCTAGGGGAGGAAGG 91

Qy        558 GCAGGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGGAGGGGTG 617
              | | ||||     | | |     |  |   |  |||||| |||| || | | | ||
Db         92 AAGGAAGGAAGGGCGGCGTGGAACGTGCTGATGGGTGGTGGCGGGGAAAATGAACGAGTA 151

Qy        618 GTCACGAATGGACGGAGGGG 637
              ||| |       ||||||
Db        152 TCCACCAGCAACGAGAGGGG 171


RESULT 14
US-09-949-016-15787
; Sequence 15787, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15787
;   LENGTH: 120727
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(120727)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15787

  Query Match             5.5%;  Score 35.4;  DB 4;  Length 120727;
  Best Local Similarity   57.8%;  Pred. No. 15;
  Matches   63;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         80 CATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAGGCAGGCCTAACTAGGTACC 139
              ||   |||  || |||  ||| |  | || |||  |  |||| ||||| |   |||  |
Db      17139 CAGCCTTTTGCTCAGCTGCTCTCTGGTTCTGTGTCGAGAAGGGAGGCCCAGTGAGGATGC 17198

Qy        140 GTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGCTGGGTTCC 188
              || |    || |||||  | || |||  | |   | ||| | | || ||
Db      17199 GTTTCGGGGAGTTTGCAGACTGCTAGGCGAGGCTGCCTAACCGAGTGCC 17247


RESULT 15
US-09-949-016-15788
; Sequence 15788, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15788
;   LENGTH: 120727
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(120727)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15788
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Query Match 5.5%; Score 35.4; DB 4; Length 120727;
Best Local Similarity 57.8%; Pred. No. 15;
Matches 63; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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Db       17139 CAGCCTTTTGCTCAGCTGCTCTCTGGTTCTGTGTCGAGAAGGGAGGCCCAGTGAGGATGC 17198

Qy         140 GTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGCTGGGTTCC 188
               || |    || |||||  | || |||  | |   | ||| | | || ||
Db       17199 GTTTCGGGGAGTTTGCAGACTGCTAGGCGAGGCTGCCTAACCGAGTGCC 17247
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Search completed: October 12, 2005, 09:35:50
Job time : 172 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 12, 2005, 09:32:55 ; Search time 2052 Seconds
(without alignments)
2168.876 Million cell updates/sec

Title: US-09-721-183-4
Perfect score: 639
Sequence: 1 ccagaaccgagtttaggtcc.....cacgaatggacggaggggat 639

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	637.4	99.7	1104	24	US-11-057-807-35	Sequence 35, Appl
3	306	47.9	307	16	US-10-082-828A-34	Sequence 34, Appl
4	306	47.9	307	24	US-11-057-807-34	Sequence 34, Appl
5	99.8	15.6	2112	17	US-10-104-047-1145	Sequence 1145, Ap
c 6	75.8	11.9	503	14	US-10-198-846-13943	Sequence 13943, A
7	45.2	7.1	202251	13	US-10-087-192-985	Sequence 985, App
c 8	42	6.6	53522	10	US-09-904-968A-1	Sequence 1, Appli
9	39.2	6.1	540	19	US-10-021-323-1875	Sequence 1875, Ap
c 10	37.4	5.9	610	13	US-10-027-632-236295	Sequence 236295,
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c 14	37.4	5.9	610	13	US-10-027-632-236299	Sequence 236299,
c 15	37.4	5.9	610	17	US-10-027-632-236295	Sequence 236295,
c 16	37.4	5.9	610	17	US-10-027-632-236296	Sequence 236296,
c 17	37.4	5.9	610	17	US-10-027-632-236297	Sequence 236297,
c 18	37.4	5.9	610	17	US-10-027-632-236298	Sequence 236298,
c 19	37.4	5.9	610	17	US-10-027-632-236299	Sequence 236299,
c 20	37.4	5.9	394468	21	US-10-741-600-17952	Sequence 17952, A
21	37.4	5.9	418550	17	US-10-292-798-1463	Sequence 1463, Ap
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c 23	37.2	5.8	1038	13	US-10-036-729-3	Sequence 3, Appli
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26	36.6	5.7	195	19	US-10-437-963-20090	Sequence 20090, A
27	36.6	5.7	976	19	US-10-437-963-8451	Sequence 8451, Ap
c 28	36.2	5.7	11263	22	US-10-756-149-3787	Sequence 3787, Ap
29	36.2	5.7	203132	19	US-10-322-281-459	Sequence 459, App
c 30	36	5.6	1599	18	US-10-425-114-33012	Sequence 33012, A
c 31	36	5.6	1599	20	US-10-425-115-141198	Sequence 141198,
c 32	35.8	5.6	592	13	US-10-027-632-280778	Sequence 280778,
c 33	35.8	5.6	592	17	US-10-027-632-280778	Sequence 280778,
c 34	35.8	5.6	735	13	US-10-027-632-26656	Sequence 26656, A
c 35	35.8	5.6	735	17	US-10-027-632-26656	Sequence 26656, A
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39	35.6	5.6	2230	17	US-10-108-260A-1530	Sequence 1530, Ap
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41	35.6	5.6	7496	15	US-10-128-714-176	Sequence 176, App
42	35.6	5.6	25751	21	US-10-741-600-17722	Sequence 17722, A
43	35.6	5.6	38753	19	US-10-741-601-5767	Sequence 5767, Ap
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ALIGNMENTS

RESULT 1
US-10-082-828A-35
; Sequence 35, Application US/10082828A
; Publication No. US20030175715A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Herve
; APPLICANT: Salceda, Susana
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
; FILE REFERENCE: DEX-0247
; CURRENT APPLICATION NUMBER: US/10/082,828A
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/243,805
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-082-828A-35

Query Match 99.7%; Score 637.4; DB 16; Length 1104;
Best Local Similarity 99.8%; Pred. No. 2.4e-194;
Matches 638; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db        526 TCCACCCCTCCACCTATGCCATGTTTTCCCTTAGCCACTCCCCAGCTCGGTGGAGGAAAG 585

Qy        121 GCAGGCCTAACTAGGTACCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGC 180
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Db        586 GCAGGCCTAACTAGGTACCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGC 645

Qy        181 TGGGTTCCAGCCACTTGTAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGGAGCAAC 240
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RESULT 2
US-11-057-807-35
; Sequence 35, Application US/11057807
; Publication No. US20050136473A1
; GENERAL INFORMATION:
;  APPLICANT: Sun, Yongming
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Salceda, Susana
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Turner, Leah
;  TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
;  FILE REFERENCE: DEX-0247
;  CURRENT APPLICATION NUMBER: US/11/057,807
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: US/10/082,828
;  PRIOR FILING DATE: 2002-07-09
;  PRIOR APPLICATION NUMBER: US 60/243,805
;  PRIOR FILING DATE: 2000-10-27
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 1104
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-057-807-35

  Query Match            99.7%;  Score 637.4;  DB 24;  Length 1104;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-194;
  Matches  638;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy        121 GCAGGCCTAACTAGGTACCGTCTTCCCGACTTTGCTCAATGATAGCTGGGTGGGTCTAGC 180
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Qy        181 TGGGTTCCAGCCACTTGTAATGTGGGACATCTCTCACCCCAACTTTGTAGGTGGAGCAAC 240
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Qy        361 AGAGATCTGAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCA 420
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RESULT 3
US-10-082-828A-34
; Sequence 34, Application US/10082828A
; Publication No. US20030175715A1
; GENERAL INFORMATION:
;  APPLICANT: Sun, Yongming
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Salceda, Susana
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Turner, Leah
;  TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
;  FILE REFERENCE: DEX-0247
;  CURRENT APPLICATION NUMBER: US/10/082,828A
;  CURRENT FILING DATE:  2002-07-09
;  PRIOR APPLICATION NUMBER: US 60/243,805
;  PRIOR FILING DATE: 2000-10-27
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 307
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n=a, c, g or t
US-10-082-828A-34
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  Query Match            47.9%;  Score 306;  DB 16;  Length 307;
  Best Local Similarity  99.7%;  Pred. No. 9.3e-88;
  Matches  306;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy        393 TGCTCTGTATCTCAATTACTGTTCTTCATTTCAATTATTCTTACCTACTATTCAGTTCCC 452
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Qy        453 TTGATCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACT 512
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Db        241 CCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACGG 300

Qy        633 AGGGGAT 639
              |||||||
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RESULT 4
US-11-057-807-34
; Sequence 34, Application US/11057807
; Publication No. US20050136473A1
; GENERAL INFORMATION:
;  APPLICANT: Sun, Yongming
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Salceda, Susana
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Turner, Leah
;  TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
;  FILE REFERENCE: DEX-0247
;  CURRENT APPLICATION NUMBER: US/11/057,807
;  CURRENT FILING DATE:  2005-02-14
;  PRIOR APPLICATION NUMBER: US/10/082,828
;  PRIOR FILING DATE: 2002-07-09
;  PRIOR APPLICATION NUMBER: US 60/243,805
;  PRIOR FILING DATE: 2000-10-27
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 307
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (28)..(28)
;   OTHER INFORMATION: n=a, c, g or t
US-11-057-807-34

  Query Match            47.9%;  Score 306;  DB 24;  Length 307;
  Best Local Similarity  99.7%;  Pred. No. 9.3e-88;
  Matches  306;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        333 GGTAAGAGAAGCATCTGTATAGGAGGCAAGAGATCTGAGTCCTTTTGAAGGCCTATCCTC 392
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 GGTAAGAGAAGCATCTGTATAGGAGGCNAGAGATCTGAGTCCTTTTGAAGGCCTATCCTC 60

Qy        393 TGCTCTGTATCTCAATTACTGTTCTTCATTTCAATTATTCTTACCTACTATTCAGTTCCC 452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCTCTGTATCTCAATTACTGTTCTTCATTTCAATTATTCTTACCTACTATTCAGTTCCC 120

Qy        453 TTGATCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACT 512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTGATCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACT 180

Qy        513 AGGAGCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATT 572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGGAGCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATT 240

Qy        573 CCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACGG 632
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Db        241 CCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACGG 300

Qy        633 AGGGGAT 639
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Db        301 AGGGGAT 307


RESULT 5
US-10-104-047-1145
; Sequence 1145, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. US20030236392A1el full length cDNA
;  FILE REFERENCE: H1-A0105
;  CURRENT APPLICATION NUMBER: US/10/104,047
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER:
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1145
;   LENGTH: 2112
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-104-047-1145

  Query Match            15.6%;  Score 99.8;  DB 17;  Length 2112;
  Best Local Similarity  89.9%;  Pred. No. 8e-21;
  Matches  107;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy        477 TCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGA 536
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TGTTGGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGACATGGGGA 220

Qy        537 GTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGG 595
              |||||||||||||||||||||||||||||||||||||||| |     | || |  ||
Db        221 GTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGATTGCTTCCTGAGGAGG 279


RESULT 6
US-10-198-846-13943/c
; Sequence 13943, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
;  APPLICANT: Lillie, James
;  APPLICANT:  Xu, Yongyao
;  APPLICANT:  Wang, Youzhen
;  APPLICANT:  Steinmann, Kathleen
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
;  TITLE OF INVENTION:  FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF BREAST CANCER
;  FILE REFERENCE: MRI-049
;  CURRENT APPLICATION NUMBER: US/10/198,846
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: 60/306,220
;  PRIOR FILING DATE: 2001-07-18
;  NUMBER OF SEQ ID NOS: 14084
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13943
;   LENGTH: 503
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
```

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;   LOCATION: 1, 500, 501, 502, 503
;   OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13943

  Query Match             11.9%;  Score 75.8;  DB 14;  Length 503;
  Best Local Similarity   97.5%;  Pred. No. 2.1e-13;
  Matches   77;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        561 GGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTC 620
              ||||||||||||||||||||||||||||||||||||||||| |||||| ||||||||||
Db        499 GGATGAAGAATTCCCTAGGTGAGGACGTGTGAGGGTGGCTGGAAGAAGGTAGGGGTGGTC 440

Qy        621 ACGAATGGACGGAGGGGAT 639
              ||||||||||||||||||
Db        439 ACGAATGGACGGAGGGGAT 421


RESULT 7
US-10-087-192-985
; Sequence 985, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  CANCER
;  FILE REFERENCE: 529452000122
;  CURRENT APPLICATION NUMBER: US/10/087,192
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 2059
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 985
;   LENGTH: 202251
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(202251)
;   OTHER INFORMATION: n = A,T,C or G
US-10-087-192-985

  Query Match              7.1%;  Score 45.2;  DB 13;  Length 202251;
  Best Local Similarity   52.7%;  Pred. No. 0.034;
  Matches   98;  Conservative    0;  Mismatches   88;  Indels    0;  Gaps    0;

Qy        452 CTTGATCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAAC 511
              | |||  || |   | | |||         | |||  |     |||| |||| ||| |
Db     140383 CCTGACATTGTGGACCTTGGGAGAAGACAGAGATCACAGTAGCAGCAGCAGCAGCAGCAG 140442

Qy        512 TAGGAGCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAAT 571
               || || ||      ||   |||| |  ||||  | |||| ||   | |||  |||| |
Db     140443 CAGCAGGAGAAAGAGGAGGAGGGGGGAAGGAGAAGGAGGAAGAGGAGGAGGGGGAAGGAG 140502

Qy        572 TCCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACG 631
                  |  ||||| | |  || | ||   |||| | |  | || ||    ||||||| |
Db     140503 AAGGAGGAAGAGGAGGAGGAAGAGGGGGAAGGAGGAAGAGGAGGAGGAAGAGAATGGAGG 140562

Qy        632 GAGGGG 637
               || ||
Db     140563 AAGAGG 140568


RESULT 8
US-09-904-968A-1/c
; Sequence 1, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
;  APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
;  APPLICANT:  GERMINO, Gregory
;  APPLICANT:  WATNICK, Terry
;  APPLICANT:  PHAKDEEKITCHAROEN, Bunyong
;  TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
;  FILE REFERENCE: JHU1680-2
;  CURRENT APPLICATION NUMBER: US/09/904,968A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/283,691
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/218,261
;  PRIOR FILING DATE: 2000-07-13
;  NUMBER OF SEQ ID NOS: 113
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 53522
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-904-968A-1

  Query Match              6.6%;  Score 42;  DB 10;  Length 53522;
  Best Local Similarity   52.9%;  Pred. No. 0.18;
  Matches   90;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy        469 GGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCACCAGAACTAGGAGCAGCCCTGAGA 528
              ||||   |    ||||   | | ||      | || |  || |   |||| ||    |||
Db      34691 GGGGAGGGGAGGAGGGGAGGAGGGAGGAGGGGAGGAGGAGGAGGGGGAGGAGGGAGGAGG 34632

Qy        529 CATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATGAAGAATTCCCTAGGTGAGGACGT 588
              | | || |  ||||  |  ||  | | || |||| | || |         | | ||||
Db      34631 GAGGAGGGGGAGGAGGAGGGGGGAGGAGGGGAGGAGGGAGGAGGGGGAGGAGGGGGACAG 34572

Qy        589 GTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAATGGACGGAGGGGA 638
              | | ||  ||   ||||| ||||||   ||  | ||  ||| || | |||
Db      34571 GAGGGGAGGGGGAGGAGAGGGGAGGAAGGGGGAGGAGGGGAGGGGGAGGA 34522


RESULT 9
US-10-021-323-1875
; Sequence 1875, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
;  APPLICANT: Deikman, Jill
;  APPLICANT:  Feng, Paul C.C.
;  APPLICANT:  Fincher, Karen L.
;  APPLICANT:  Ziegler, Todd E.
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(52274)B
;  CURRENT APPLICATION NUMBER: US/10/021,323
;  CURRENT FILING DATE:  2001-12-12
;  PRIOR APPLICATION NUMBER: US 60/255, 619
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 1875
;   LENGTH: 540
;   TYPE: DNA
;   ORGANISM: Gossypium hirsutum
;   FEATURE:
;   OTHER INFORMATION: Clone ID: LIB3825-006-Q1-N6-H8
US-10-021-323-1875

  Query Match              6.1%;  Score 39.2;  DB 19;  Length 540;
  Best Local Similarity   47.2%;  Pred. No. 0.14;
  Matches  119;  Conservative    0;  Mismatches  133;  Indels    0;  Gaps    0;

Qy        386 TATCCTCTGCTCTGTATCTCAATTACTGTTCTTCATTTCAATTATTCTTACCTACTATTC 445
              | |  | |  | | | | |   ||  | || ||  ||| | || || |||  || |  |
Db         19 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTATTTATTTATT 78

Qy        446 AGTTCCCTTGATCTTTTCTTCTTGGGGGCTGTCTTAGGGTCAGGGAGATTGCAGAAGCAC 505
              |||   ||  | ||||  | || |    ||| |   |   || | |   |   |||||
Db         79 TGTTTATTTTTTGTTTTTATTTTTGTTTTTGTTTATAGAAAAGAGGGTGGGGGAAAGCAG 138

Qy        506 CAGAACTAGGAGCAGCCCTGAGACATGGGGAGTTGGAGCTGAAGGAGGAATGGCAGGATG 565
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Db        139 TGGCGAAAGGGGGGGGGGGGGGGAAGGGGGGGGGGGAAGGGGGGGGGGGAGAAGGGGGG 198

Qy        566 AAGAATTCCCTAGGTGAGGACGTGTGAGGGTGGCTGGGAGAAGGGAGGGGTGGTCACGAA 625

Db        199 AAAAAGGGGGGGGGGGGGGAAAAAGGGGCAAACCGGGAGAAGAAAAAGAGGGAAACAAA 258

Qy        626 TGGACGGAGGGG 637

Db        259 AAAAACAAAGGG 270


RESULT 10
US-10-027-632-236295/c
; Sequence 236295, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 236295
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(610)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-236295

  Query Match             5.9%;  Score 37.4;  DB 13;  Length 610;
  Best Local Similarity   52.2%;  Pred. No. 0.56;
  Matches   83;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy        309 AATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGCAAGAGATCT 368

Db        565 AGTTTCCCTTTAGCCAAGGAAGAAGGAAAAAAAATGAATGCATAGAGATCCATGTAGATCA 506

Qy        369 GAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCATTTCAATT 428

Db        505 GTGGCTCTTGAATTCTTTATCCTAAGATCTGTTTCTCTCATTCTATGCTTCCTATCCCAC 446

Qy        429 ATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCT 467

Db        445 AGTTTGGCATTCTTAAATTTTCCCAACTCCTATATTTAT 407


RESULT 11
US-10-027-632-236296/c
; Sequence 236296, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 236296
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(610)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-236296

  Query Match             5.9%;  Score 37.4;  DB 13;  Length 610;
  Best Local Similarity   52.2%;  Pred. No. 0.56;
  Matches   83;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy        309 AATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGCAAGAGATCT 368

Db        565 AGTTTCCCTTTAGCCAAGGAAGAAGGAAAAAAAATGAATGCATAGAGATCCATGTAGATCA 506

Qy        369 GAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCATTTCAATT 428

Db        505 GTGGCTCTTGAATTCTTTATCCTAAGATCTGTTTCTCTCATTCTATGCTTCCTATCCCAC 446

Qy        429 ATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCT 467

Db        445 AGTTTGGCATTCTTAAATTTTCCCAACTCCTATATTTAT 407


RESULT 12
US-10-027-632-236297/c
; Sequence 236297, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 236297
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(610)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-236297

  Query Match             5.9%;  Score 37.4;  DB 13;  Length 610;
  Best Local Similarity   52.2%;  Pred. No. 0.56;
  Matches   83;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy        309 AATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGCAAGAGATCT 368
              | | | | | |||| | |  ||||| || | | | ||   || ||        |||||
Db        565 AGTTTCCCTTTAGCCAAGGAAGAAGGAAAAAAATGAATGCATAGAGATCCATGTAGATCA 506

Qy        369 GAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCATTTCAATT 428
              | | |  ||  |     ||||||  | ||||| ||||   | || | |||| | ||
Db        505 GTGGCTCTTGAATTCTTTATCCTAAGATCTGTTTCTCTCATTCTATGCTTCCTATCCCAC 446

Qy        429 ATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCT 467
              | | |  | | ||      |||||     || |  || |
Db        445 AGTTTGGCATTCTTAAATTTTCCCAACTCCTATATTTAT 407


RESULT 13
US-10-027-632-236298/c
; Sequence 236298, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 236298
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(610)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-236298

  Query Match             5.9%;  Score 37.4;  DB 13;  Length 610;
  Best Local Similarity   52.2%;  Pred. No. 0.56;
  Matches   83;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy        309 AATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGCAAGAGATCT 368
              | | | | | |||| | |  ||||| || | | | ||   || ||        |||||
Db        565 AGTTTCCCTTTAGCCAAGGAAGAAGGAAAAAAATGAATGCATAGAGATCCATGTAGATCA 506

Qy        369 GAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCATTTCAATT 428
              | | |  ||  |     ||||||  | ||||| ||||   | || | |||| | ||
Db        505 GTGGCTCTTGAATTCTTTATCCTAAGATCTGTTTCTCTCATTCTATGCTTCCTATCCCAC 446

Qy        429 ATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCT 467
              | | |  | | ||      |||||     || |  || |
Db        445 AGTTTGGCATTCTTAAATTTTCCCAACTCCTATATTTAT 407


RESULT 14
US-10-027-632-236299/c
; Sequence 236299, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 236299
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(610)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-236299

  Query Match             5.9%;  Score 37.4;  DB 13;  Length 610;
  Best Local Similarity   52.2%;  Pred. No. 0.56;
  Matches   83;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy        309 AATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGCAAGAGATCT 368
              | | | | | |||| | |  ||||| || | | | ||   || ||        |||||
Db        565 AGTTTCCCTTTAGCCAAGGAAGAAGGAAAAAAATGAATGCATAGAGATCCATGTAGATCA 506

Qy        369 GAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCATTTCAATT 428
              | | |  ||  |     ||||||  | ||||| ||||   | || | |||| | ||
Db        505 GTGGCTCTTGAATTCTTTATCCTAAGATCTGTTTCTCTCATTCTATGCTTCCTATCCCAC 446

Qy        429 ATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCT 467
              | | |  | | ||      |||||     || |  || |
Db        445 AGTTTGGCATTCTTAAATTTTCCCAACTCCTATATTTAT 407


RESULT 15
US-10-027-632-236295/c
; Sequence 236295, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
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;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 236295
;   LENGTH: 610
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(610)
;   OTHER INFORMATION: n = A,T,C or G
US-10-027-632-236295

  Query Match             5.9%;  Score 37.4;  DB 17;  Length 610;
  Best Local Similarity   52.2%;  Pred. No. 0.56;
  Matches   83;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy        309 AATCTGCTTCTAGCAAGTGGTGAAGGTAAGAGAAGCATCTGTATAGGAGGCAAGAGATCT 368
              | | | | | |||| |  |  ||||| || | | | ||   || ||        |||||
Db r      565 AGTTTCCCTTTAGCCAAGGAAGAAGGAAAAAAATGAATGCATAGAGATCCATGTAGATCA 506

Qy        369 GAGTCCTTTTGAAGGCCTATCCTCTGCTCTGTATCTCAATTACTGTTCTTCATTTCAATT 428
              | | |  ||  |     ||||||  | ||||| ||||   | || | |||| | ||
Db  t     505 GTGGCTCTTGAATTCTTTATCCTAAGATCTGTTTCTCTCATTCTATGCTTCCTATCCCAC 446

Qy        429 ATTCTTACCTACTATTCAGTTCCCTTGATCTTTTCTTCT 467
              | | |  | | ||       |||||     || |  || |
Db        445 AGTTTGGCATTCTTAAATTTTCCCAACTCCTATATTTAT 407


Search completed: October 12, 2005, 10:18:19
Job time : 2054 secs
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